

## Raw Sequence Listing Error Summary

| <b><u>ERROR DETECTED</u></b> | <b><u>SUGGESTED CORRECTION</u></b> |
|------------------------------|------------------------------------|
|------------------------------|------------------------------------|

SERIAL NUMBER: 09/129,958

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- |    |      |                                  |   |
|----|------|----------------------------------|---|
| 1  | ____ | Wrapped Nucleics                 | The number/text at the end of each line "wrapped" down to the next line.<br>This may occur if your file was retrieved in a word processor after creating it.<br>Please adjust your right margin to .3, as this will prevent "wrapping".   |
| 2  | ____ | Wrapped Aminos                   | The amino acid number/text at the end of each line "wrapped" down to the next line.<br>This may occur if your file was retrieved in a word processor after creating it.<br>Please adjust your right margin to .3, as this will prevent "wrapping".  |
| 3  | ____ | Incorrect Line Length            | The rules require that a line not exceed 72 characters in length. This includes spaces.   |
| 4  | ____ | Misaligned Amino Acid Numbering  | The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.   |
| 5  | ____ | Non-ASCII                        | This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.<br>Please ensure your subsequent submission is saved in ASCII text so that it can be processed.   |
| 6  | ____ | Variable Length                  | Sequence(s) ____ contain n's or Xaa's which represented more than one residue.<br>As per the rules, each n or Xaa can only represent a single residue.<br>Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.   |
| 7  | ____ | PatentIn ver. 2.0 "bug"          | A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence.  |
| 8  | ____ | Skipped Sequences (OLD RULES)    | Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:<br><b>(2) INFORMATION FOR SEQ ID NO:X:</b><br><b>(i) SEQUENCE CHARACTERISTICS:</b> (Do not insert any headings under "SEQUENCE CHARACTERISTICS")<br><b>(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:</b><br><b>This sequence is intentionally skipped</b><br><br>Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s). |
| 9  | ____ | Skipped Sequences (NEW RULES)    | Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence.<br><b>&lt;210&gt; sequence id number</b><br><b>&lt;400&gt; sequence id number</b><br><b>000</b>  |
| 10 | ✓    | Use of n's or Xaa's (NEW RULES)  | Use of n's and/or Xaa's have been detected in the Sequence Listing.<br>Use of <220> to <223> is MANDATORY if n's or Xaa's are present.<br>In <220> to <223> section, please explain location of n or Xaa, and <u>which residue n or Xaa represents.</u>   |
| 11 | ____ | Use of <213>Organism (NEW RULES) | Sequence(s) _____ are missing this mandatory field or its response.   |
| 12 | ____ | Use of <220>Feature (NEW RULES)  | Sequence(s) ____ are missing the <220>Feature and associated headings.<br>Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"<br><b>Please explain source of genetic material in &lt;220&gt; to &lt;223&gt; section.</b><br><b>(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)</b>   |
| 13 | ____ | PatentIn ver. 2.0 "bug"          | <b>Please do not use "Copy to Disk" function of PatentIn version 2.0.</b> This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.   |

AKS-Biotechnology Systems Branch- 5/15/99

- Fredman

1655

PAGE: 1

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/129,958

DATE: 07/20/1999  
TIME: 16:36:07

Input Set: I129958.RAW

This Raw Listing contains the General Information  
Section and up to first 5 pages.

Does Not Comply  
Corrected Diskette Needed

1 <110> APPLICANT: Mills, Allen P.  
2 Yurke, Bernard  
3 Platzman, Philip M.  
4 <120> TITLE OF INVENTION: ANALOG AND NEURAL NETWORK COMPUTATION USING DNA  
5 <130> FILE REFERENCE: LUTEC 0008  
6 <140> CURRENT APPLICATION NUMBER: US/09/129,958  
7 <141> CURRENT FILING DATE: 1998-08-06  
8 <150> EARLIER APPLICATION NUMBER: 09/078,761  
9 <151> EARLIER FILING DATE: 1998-05-15  
10 <150> EARLIER APPLICATION NUMBER: 09/018,248  
11 <151> EARLIER FILING DATE: 1998-02-03  
12 <150> EARLIER APPLICATION NUMBER: 60/086,654  
13 <151> EARLIER FILING DATE: 1998-05-26  
14 <160> NUMBER OF SEQ ID NOS: 4  
15 <170> SOFTWARE: PatentIn Ver. 2.0  
16 <210> SEQ ID NO 1  
17 <211> LENGTH: 10  
18 <212> TYPE: DNA  
19 <213> ORGANISM: Artificial Sequence  
20 <220> FEATURE:  
21 <223> OTHER INFORMATION: Description of Artificial Sequence: DNA based  
22 analog oligonucleotide  
23 <400> SEQUENCE: 1  
24 agctatcgat 10  
25 <210> SEQ ID NO 2  
26 <211> LENGTH: 34  
27 <212> TYPE: DNA  
28 <213> ORGANISM: Artificial Sequence  
29 <220> FEATURE:  
30 <223> OTHER INFORMATION: Description of Artificial Sequence: DNA based  
31 analog oligonucleotide  
32 <220> FEATURE:  
33 <221> NAME/KEY: variation  
34 <222> LOCATION: (34)  
35 <400> SEQUENCE: 2  
36 aatgcaagat cgaaatttat acgtttatct tach) 34  
37 <210> SEQ ID NO 3  
38 <211> LENGTH: 34  
39 <212> TYPE: DNA  
40 <213> ORGANISM: Artificial Sequence  
41 <220> FEATURE:  
42 <223> OTHER INFORMATION: Description of Artificial Sequence: DNA based  
43 analog oligonucleotide  
44 <220> FEATURE:

W-->

an explanation of "h" is mandatory  
in <223> response  
(see item 10 on  
Eva summary sheet)  
and see 1,823 of sequence  
Ruber)

PAGE: 2

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/129,958DATE: 07/20/1999  
TIME: 16:36:07

Input Set: I129958.RAW

45 <221> NAME/KEY: variation  
46 <222> LOCATION: (34)  
47 <400> SEQUENCE: 3  
W--> 48 *same error*  
aatgcaagat cgaaatttat acgtttatct ta<sup>o</sup> 34  
49 <210> SEQ ID NO 4  
50 <211> LENGTH: 30  
51 <212> TYPE: DNA  
52 <213> ORGANISM: Artificial Sequence  
53 <220> FEATURE:  
54 <223> OTHER INFORMATION: Description of Artificial Sequence: DNA based  
55 analog oligonucleotide  
56 <400> SEQUENCE: 4  
57 aatgcaagat cgaaatttat acgtttatct 30

VERIFICATION SUMMARY  
PATENT APPLICATION US/09/129,958DATE: 07/20/1999  
TIME: 16:36:07

Input Set: I129958.RAW

| Line | Error/Warning                       | Original Text                         |
|------|-------------------------------------|---------------------------------------|
| 36 W | "N" or "Xaa" used: Feature required | aatgcaagat cgaaatttat acgtttatct tacn |
| 48 W | "N" or "Xaa" used: Feature required | aatgcaagat cgaaatttat acgtttatct tacn |